

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Sheppard, Paul O.
- (ii) TITLE OF THE INVENTION: SERINE PROTEASE POLYPEPTIDES
AND MATERIALS AND METHODS FOR MAKING THEM
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: ZymoGenetics, Inc.
(B) STREET: 1201 Eastlake Avenue East
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98102
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Parker, Gary E
(B) REGISTRATION NUMBER: 31,648
(C) REFERENCE/DOCKET NUMBER: 97-16
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 206-442-6673
(B) TELEFAX: 206-442-6678
(C) TELEX:

B62T40: 2729060

| | | | | | | | |
|---|------------|------------|------------|----------------------|------------|-----|----|
| GGCACGAGGG | GGAGCCGCGC | GCTCTCTCCC | GGCGCCACAC | CCTGTCTGAG | CGGCGCAGCG | | 60 |
| AGCCGCGGCC | CGGGCGGGCT | GCTCGGCGCG | GAACAGTGCT | CGGC ATG GCA GGG ATT | | 116 | |
| | | | | Met Ala Gly Ile | | | |
| | | | | | | | |
| CCA GGG CTC CTC TTC CTT CTC TTC TTT CTG CTC TGT GCT GTT GGG CAA | | 164 | | | | | |
| Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys Ala Val Gly Gln | | | | | | | |
| -15 | -10 | -5 | 1 | | | | |
| | | | | | | | |
| GTG AGC CCT TAC AGT GCC CCC TGG AAA CCC ACT TGG CCT GCA TAC CGC | | 212 | | | | | |
| Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp Pro Ala Tyr Arg | | | | | | | |
| | 5 | 10 | 15 | | | | |
| | | | | | | | |
| CTC CCT GTC GTC TTG CCC CAG TCT ACC CTC AAT TTA GCC AAG CCA GAC | | 260 | | | | | |
| Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu Ala Lys Pro Asp | | | | | | | |
| | 20 | 25 | 30 | | | | |
| | | | | | | | |
| TTT GGA GCC GAA GCC AAA TTA GAA GTA TCT TCT TCA TGT GGA CCC CAG | | 308 | | | | | |
| Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser Cys Gly Pro Gln | | | | | | | |
| 35 | 40 | 45 | | | | | |
| | | | | | | | |
| TGT CAT AAG GGA ACT CCA CTG CCC ACT TAC AAA GAA GCC AAG CAA TAT | | 356 | | | | | |
| Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Lys Glu Ala Lys Gln Tyr | | | | | | | |
| 50 | 55 | 60 | 65 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTG | TCT | TAT | GAA | ACG | CTC | TAT | GCC | AAT | GGC | AGC | CGC | ACA | GAG | ACN | CAG | 404 |
| Leu | Ser | Tyr | Glu | Thr | Leu | Tyr | Ala | Asn | Gly | Ser | Arg | Thr | Glu | Xaa | Gln | |
| | | | | 70 | | | | | 75 | | | | | 80 | | |
| GTG | GGC | ATC | TAC | ATC | CTC | AGC | AGT | AGT | GGA | GAT | GGG | GCC | CAN | CNC | CGA | 452 |
| Val | Gly | Ile | Tyr | Ile | Leu | Ser | Ser | Ser | Gly | Asp | Gly | Ala | Xaa | Xaa | Arg | |
| | | | 85 | | | | | 90 | | | | | 95 | | | |
| GAC | TCA | GGG | TCT | TCA | GGA | AAG | TCT | CGA | AGG | AAG | CGG | CAG | ATT | TAT | GGC | 500 |
| Asp | Ser | Gly | Ser | Ser | Gly | Lys | Ser | Arg | Arg | Lys | Arg | Gln | Ile | Tyr | Gly | |
| | | 100 | | | | | 105 | | | | | 110 | | | | |
| TAT | GAC | AGC | AGG | TTC | AGC | ATT | TTT | GGG | AAG | GAC | TTC | CTG | CTC | AAC | TAC | 548 |
| Tyr | Asp | Ser | Arg | Phe | Ser | Ile | Phe | Gly | Lys | Asp | Phe | Leu | Leu | Asn | Tyr | |
| | 115 | | | | | 120 | | | | | 125 | | | | | |
| CCT | TTC | TCA | ACA | TCA | GTG | AAG | TTA | TCC | ACG | GGC | TGC | ACC | GGC | ACC | CTG | 596 |
| Pro | Phe | Ser | Thr | Ser | Val | Lys | Leu | Ser | Thr | Gly | Cys | Thr | Gly | Thr | Leu | |
| 130 | | | | | 135 | | | | | 140 | | | | | 145 | |
| GTG | GCA | GAA | AAN | CAT | GTC | CTC | ACA | GCT | GCC | CAC | TGC | ATA | CAC | GAT | GGA | 644 |
| Val | Ala | Glu | Xaa | His | Val | Leu | Thr | Ala | Ala | His | Cys | Ile | His | Asp | Gly | |
| | | | | 150 | | | | | 155 | | | | | 160 | | |
| AAA | ACC | TAT | GTG | AAA | GGA | ACC | CAG | AAG | CTT | CGA | GTC | GGC | TTC | CTA | AAG | 692 |
| Lys | Thr | Tyr | Val | Lys | Gly | Thr | Gln | Lys | Leu | Arg | Val | Gly | Phe | Leu | Lys | |
| | | | 165 | | | | | 170 | | | | | 175 | | | |
| CCC | AAG | TTT | AAA | GAT | GGT | GGT | CGA | GGG | GCC | AAC | GAC | TCC | ACT | TCA | GCC | 740 |
| Pro | Lys | Phe | Lys | Asp | Gly | Gly | Arg | Gly | Ala | Asn | Asp | Ser | Thr | Ser | Ala | |
| | | 180 | | | | | 185 | | | | | 190 | | | | |
| ATG | CCC | GAG | CAG | ATG | AAA | TTT | CAG | TGG | ATC | CGG | GTG | AAA | CGC | ACC | CAT | 788 |
| Met | Pro | Glu | Gln | Met | Lys | Phe | Gln | Trp | Ile | Arg | Val | Lys | Arg | Thr | His | |
| | 195 | | | | | 200 | | | | | 205 | | | | | |
| GTG | CCC | AAG | GGT | TGG | ATC | AAG | GGC | AAT | GCC | AAT | GAC | ATC | GGC | ATG | GAT | 836 |
| Val | Pro | Lys | Gly | Trp | Ile | Lys | Gly | Asn | Ala | Asn | Asp | Ile | Gly | Met | Asp | |
| 210 | | | | | 215 | | | | 220 | | | | | 225 | | |
| TAT | GAT | TAT | GCC | CTC | CTG | GAA | CTC | AAA | AAG | CCC | CAC | AAG | AGA | AAA | TTT | 884 |
| Tyr | Asp | Tyr | Ala | Leu | Leu | Glu | Leu | Lys | Lys | Pro | His | Lys | Arg | Lys | Phe | |
| | | | | 230 | | | | | 235 | | | | | 240 | | |

ATG AAG ATT GGG GTG AGC CCT CCT GCT AAG CAG CTG CCA GGG GGC AGA 932
 Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu Pro Gly Gly Arg
 245 250 255

ATT CAC TTC TCT GGT TAT GAC AAT GAC CGA CCA GGC AAT TTG GTG TAT 980
 Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly Asn Leu Val Tyr
 260 265 270

CGC TTC TGT GAC GTC AAA GAC GAG ACC TAT GAC TTG TTG TAC CAG CAA 1028
 Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu Leu Tyr Gln Gln
 275 280 285

TGC GAT GCC CAG CCA GGG GCC AGC GGG TAT GGG GTA TAT GTG AGG ATG 1076
 Cys Asp Ala Gln Pro Gly Ala Ser Gly Tyr Gly Val Tyr Val Arg Met
 290 295 300 305

TGG AAG AGA CAG CAG CAG AAG TGG GAG CGA AAA ATT ATT GGC ATT TTT 1124
 Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe
 310 315 320

TCA GGG CAC CAG TGG GTG GAC ATG AAT GGT TCC CCA CAG GAT TTC AAC 1172
 Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn
 325 330 335

GTG GCT GTC AGA ATC ACT CCT CTC AAA TAT GCC CAG ATC TGC TAT TGG 1220
 Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp
 340 345 350

ATT AAA GGA AAC TAC CTG GAT TGT AGG GAG GGT GAC ACA GTG TTC CTT 1268
 Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp Thr Val Phe Leu
 355 360 365

CCT GGC AGC AAT TAAGGTCTTC ATGTTCTTAT TTAGGAGAG GCCAAATTGT TTTT 1325
 Pro Gly Ser Asn
 370

GTCATTGGCG TGCACACGTG TGTGTGTGTG TGTGTGTGTG TGTAAGGTGT CTTATAATCT 1385
 TTTACCTATT TCTTACAATT GCAAGATGAC TGGCTTTACT ATTTGAAAAC TGGTTTGTGT 1445
 ATCATATCAT ATATCATTTA AGCAGTTTGA AGGCATACTT TTGCATAGAA ATAAAAAAAA 1505
 TACTGATTTG GGGCAATGAG GAATATTTGA CAATTAAGTT AATCTTCACG TTTTGTGCAA 1565
 CTTTGATTTT TATTTCTCT GAACTTGTTT CAAAGATTTA TATTAAATAT TTGGCATACA 1625
 AGAGATATG 1634

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

8521410-24729060

(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|-----------|-----|
| Met | Ala | Gly | Ile | Pro -15 | Gly | Leu | Leu | Phe | Leu -10 | Leu | Phe | Phe | Leu | Leu -5 | Cys |
| Ala | Val | Gly | Gln | Val | Ser | Pro | Tyr | Ser | Ala | Pro | Trp | Lys | Pro | Thr | Trp |
| | | | 1 | | | | 5 | | | | | 10 | | | |
| Pro | Ala | Tyr | Arg | Leu | Pro | Val | Val | Leu | Pro | Gln | Ser | Thr | Leu | Asn | Leu |
| | 15 | | | | | 20 | | | | | 25 | | | | |
| Ala | Lys | Pro | Asp | Phe | Gly | Ala | Glu | Ala | Lys | Leu | Glu | Val | Ser | Ser | Ser |
| 30 | | | | | 35 | | | | | 40 | | | | | 45 |
| Cys | Gly | Pro | Gln | Cys | His | Lys | Gly | Thr | Pro | Leu | Pro | Thr | Tyr | Lys | Glu |
| | | | | 50 | | | | | 55 | | | | | 60 | |
| Ala | Lys | Gln | Tyr | Leu | Ser | Tyr | Glu | Thr | Leu | Tyr | Ala | Asn | Gly | Ser | Arg |
| | | | 65 | | | | | 70 | | | | | 75 | | |
| Thr | Glu | Xaa | Gln | Val | Gly | Ile | Tyr | Ile | Leu | Ser | Ser | Ser | Gly | Asp | Gly |
| | | 80 | | | | | 85 | | | | | | 90 | | |
| Ala | Xaa | Xaa | Arg | Asp | Ser | Gly | Ser | Ser | Gly | Lys | Ser | Arg | Arg | Lys | Arg |
| | 95 | | | | | 100 | | | | | 105 | | | | |
| Gln | Ile | Tyr | Gly | Tyr | Asp | Ser | Arg | Phe | Ser | Ile | Phe | Gly | Lys | Asp | Phe |
| 110 | | | | | 115 | | | | | 120 | | | | | 125 |
| Leu | Leu | Asn | Tyr | Pro | Phe | Ser | Thr | Ser | Val | Lys | Leu | Ser | Thr | Gly | Cys |
| | | | | 130 | | | | | 135 | | | | | 140 | |
| Thr | Gly | Thr | Leu | Val | Ala | Glu | Xaa | His | Val | Leu | Thr | Ala | Ala | His | Cys |
| | | | 145 | | | | | 150 | | | | | 155 | | |
| Ile | His | Asp | Gly | Lys | Thr | Tyr | Val | Lys | Gly | Thr | Gln | Lys | Leu | Arg | Val |
| | | 160 | | | | | 165 | | | | | 170 | | | |
| Gly | Phe | Leu | Lys | Pro | Lys | Phe | Lys | Asp | Gly | Gly | Arg | Gly | Ala | Asn | Asp |
| | 175 | | | | | 180 | | | | | 185 | | | | |
| Ser | Thr | Ser | Ala | Met | Pro | Glu | Gln | Met | Lys | Phe | Gln | Trp | Ile | Arg | Val |
| 190 | | | | | 195 | | | | | 200 | | | | | 205 |
| Lys | Arg | Thr | His | Val | Pro | Lys | Gly | Trp | Ile | Lys | Gly | Asn | Ala | Asn | Asp |
| | | | | 210 | | | | | 215 | | | | | 220 | |

Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His
 225 230 235
 Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
 240 245 250
 Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly
 255 260 265
 Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu
 270 275 280 285
 Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Tyr Gly Val
 290 295 300
 Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile
 305 310 315
 Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro
 320 325 330
 Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln
 335 340 345
 Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp
 350 355 360 365
 Thr Val Phe Leu Pro Gly Ser Asn
 370

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGYACNGGNW SNHTNRT

17

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AYNADNSWNC CNGTRCA

17

962740: 2729060

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACNGCNGSNC AYTGYAT

17

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATRCARTGNS CNGCNGT

17

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

WYRTNCCNWW NGGNTGG

17

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

AYNRAYTAYG AYTAYGS

17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

SCRTARTCRT ARTYNRT

17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZC11667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

(A) NAME/KEY: Signal Sequence
(B) LOCATION: 105...161
(D) OTHER INFORMATION:

GGCACGAGGG GGAGCCGCGC GCTCTCTCCC GGCGCCCACA CCTGTCTGAG CGGCGCAGCG 60
AGCCGCGGCC CGGGCGGGCT GCTCGGCGCG GAACAGTGCT CGGC ATG GCA GGG ATT 116
Met Ala Gly Ile

CCA GGG CTC CTC TTC CTT CTC TTC TTT CTG CTC TGT GCT GTT GGG CAA 164
Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys Ala Val Gly Gln
-15 -10 -5 1

GTG AGC CCT TAC AGT GCC CCC TGG AAA CCC ACT TGG CCT GCA TAC CGC 212
Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp Pro Ala Tyr Arg
5 10 15

CTC CCT GTC GTC TTG CCC CAG TCT ACC CTC AAT TTA GCC AAG CCA GAC 260
Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu Ala Lys Pro Asp
20 25 30

TTT GGA GCC GAA GCC AAA TTA GAA GTA TCT TCT TCA TGT GGA CCC CAG 308
Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser Cys Gly Pro Gln
35 40 45

TGT CAT AAG GGA ACT CCA CTG CCC ACT TAC GAA GAG GCC AAG CAA TAT 356
Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu Ala Lys Gln Tyr
50 55 60 65

CTG TCT TAT GAA ACG CTC TAT GCC AAT GGC AGC CGC ACA GAG ACG CAG 404
Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln
70 75 80

GTG GGC ATC TAC ATC CTC AGC AGT AGT GGA GAT GGG GCC CAA CAC CGA 452
Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg
85 90 95

GAC TCA GGG TCT TCA GGA AAG TCT CGA AGG AAG CGG CAG ATT TAT GGC 500
Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly
100 105 110

| | | | | | | | | | | | | | | | | |
|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| TAT Tyr | GAC Asp | AGC Ser | AGG Arg | TTC Phe | AGC Ser | ATT Ile | TTT Phe | GGG Gly | AAG Lys | GAC Asp | TTC Phe | CTG Leu | CTC Leu | AAC Asn | TAC Tyr | 548 |
| 115120125 | | | | | | | | | | | | | | | | |
| CCT Pro | TTC Phe | TCA Ser | ACA Thr | TCA Ser | GTG Val | AAG Lys | TTA Leu | TCC Ser | ACG Thr | GGC Gly | TGC Cys | ACC Thr | GGC Gly | ACC Thr | CTG Leu | 596 |
| 130135140145 | | | | | | | | | | | | | | | | |
| GTG Val | GCA Ala | GAG Glu | AAG Lys | CAT His | GTC Val | CTC Leu | ACA Thr | GCT Ala | GCC Ala | CAC His | TGC Cys | ATA Ile | CAC His | GAT Asp | GGA Gly | 644 |
| 150155160 | | | | | | | | | | | | | | | | |
| AAA Lys | ACC Thr | TAT Tyr | GTG Val | AAA Lys | GGA Gly | ACC Thr | CAG Gln | AAG Lys | CTT Leu | CGA Arg | GTG Val | GGC Gly | TTC Phe | CTA Leu | AAG Lys | 692 |
| 165170175 | | | | | | | | | | | | | | | | |
| CCC Pro | AAG Lys | TTT Phe | AAA Lys | GAT Asp | GGT Gly | GGT Gly | CGA Arg | GGG Gly | GCC Ala | AAC Asn | GAC Asp | TCC Ser | ACT Thr | TCA Ser | GCC Ala | 740 |
| 180185190 | | | | | | | | | | | | | | | | |
| ATG Met | CCC Pro | GAG Glu | CAG Gln | ATG Met | AAA Lys | TTT Phe | CAG Gln | TGG Trp | ATC Ile | CGG Arg | GTG Val | AAA Lys | CGC Arg | ACC Thr | CAT His | 788 |
| 195200205 | | | | | | | | | | | | | | | | |
| GTG Val | CCC Pro | AAG Lys | GGT Gly | TGG Trp | ATC Ile | AAG Lys | GGC Gly | AAT Asn | GCC Ala | AAT Asn | GAC Asp | ATC Ile | GGC Gly | ATG Met | GAT Asp | 836 |
| 210215220225 | | | | | | | | | | | | | | | | |
| TAT Tyr | GAT Asp | TAT Tyr | GCC Ala | CTC Leu | CTG Leu | GAA Glu | CTC Leu | AAA Lys | AAG Lys | CCC Pro | CAC His | AAG Lys | AGA Arg | AAA Lys | TTT Phe | 884 |
| 230235240 | | | | | | | | | | | | | | | | |
| ATG Met | AAG Lys | ATT Ile | GGG Gly | GTG Val | AGC Ser | CCT Pro | CCT Pro | GCT Ala | AAG Lys | CAG Gln | CTG Leu | CCA Pro | GGG Gly | GGC Gly | AGA Arg | 932 |
| 245250255 | | | | | | | | | | | | | | | | |
| ATT Ile | CAC His | TTC Phe | TCT Ser | GGT Gly | TAT Tyr | GAC Asp | AAT Asn | GAC Asp | CGA Arg | CCA Pro | GGC Gly | AAT Asn | TTG Leu | GTG Val | TAT Tyr | 980 |
| 260265270 | | | | | | | | | | | | | | | | |
| CGC Arg | TTC Phe | TGT Cys | GAC Asp | GTC Val | AAA Lys | GAC Asp | GAG Glu | ACC Thr | TAT Tyr | GAC Asp | TTG Leu | CTC Leu | TAC Tyr | CAG Gln | CAA Gln | 1028 |
| 275280285 | | | | | | | | | | | | | | | | |

TGC GAT GCC CAG CCA GGG GCC AGC GGG TCT GGG GTC TAT GTG AGG ATG 1076
 Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val Tyr Val Arg Met
 290 295 300 305

TGG AAG AGA CAG CAG CAG AAG TGG GAG CGA AAA ATT ATT GGC ATT TTT 1124
 Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe
 310 315 320

TCA GGG CAC CAG TGG GTG GAC ATG AAT GGT TCC CCA CAG GAT TTC AAC 1172
 Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn
 325 330 335

GTG GCT GTC AGA ATC ACT CCT CTC AAA TAT GCC CAG ATC TGC TAT TGG 1220
 Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp
 340 345 350

ATT AAA GGA AAC TAC CTG GAT TGT AGG GAG GGT GAC ACA GTG TTC CCT 1268
 Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp Thr Val Phe Pro
 355 360 365

CCT GGC AGC AAT TAAGGTCTTC ATGTTCTTAT TTTAGGAGAG GCCAAATTGT TTTTT 1325
 Pro Gly Ser Asn
 370

GTCATTGGCG TGCACACGTG TGTGTGTGTG TGTGTGTGTG TGTAAGGTGT CTTATAATCT 1385
 TTTACCTATT TCTTACAATT GCAAGATGAC TGGCTTTACT ATTTGAAAAC TGGTTTGTGT 1445
 ATCATATCAT ATATCATTTA AGCAGTTTGA AGGCATACTT TTGCATAGAA ATAAAAAAAA 1505
 TACTGATTTG GGGCAATGAG GAATATTTGA CAATTAAGTT AATCTTCACG TTTTGTGCAA 1565
 CTTTGATTTT TATTTTCATCT GAACTTGTTT CAAAGATTTA TATTAAATAT TTGGCATACA 1625
 AGAGATATGA AAAAAAAAAA AAAAAAAAAA A 1656

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Ile | Pro | Gly | Leu | Leu | Phe | Leu | Leu | Phe | Phe | Leu | Leu | Cys |
| | | | | -15 | | | | | -10 | | | | | -5 | |
| Ala | Val | Gly | Gln | Val | Ser | Pro | Tyr | Ser | Ala | Pro | Trp | Lys | Pro | Thr | Trp |
| | | | 1 | | | | 5 | | | | | 10 | | | |
| Pro | Ala | Tyr | Arg | Leu | Pro | Val | Val | Leu | Pro | Gln | Ser | Thr | Leu | Asn | Leu |
| | 15 | | | | | 20 | | | | | 25 | | | | |
| Ala | Lys | Pro | Asp | Phe | Gly | Ala | Glu | Ala | Lys | Leu | Glu | Val | Ser | Ser | Ser |
| 30 | | | | | 35 | | | | | 40 | | | | | 45 |
| Cys | Gly | Pro | Gln | Cys | His | Lys | Gly | Thr | Pro | Leu | Pro | Thr | Tyr | Glu | Glu |
| | | | | 50 | | | | | 55 | | | | | 60 | |
| Ala | Lys | Gln | Tyr | Leu | Ser | Tyr | Glu | Thr | Leu | Tyr | Ala | Asn | Gly | Ser | Arg |
| | | | 65 | | | | | 70 | | | | | 75 | | |
| Thr | Glu | Thr | Gln | Val | Gly | Ile | Tyr | Ile | Leu | Ser | Ser | Ser | Gly | Asp | Gly |
| | | 80 | | | | | 85 | | | | | 90 | | | |
| Ala | Gln | His | Arg | Asp | Ser | Gly | Ser | Ser | Gly | Lys | Ser | Arg | Arg | Lys | Arg |
| | 95 | | | | | 100 | | | | | 105 | | | | |
| Gln | Ile | Tyr | Gly | Tyr | Asp | Ser | Arg | Phe | Ser | Ile | Phe | Gly | Lys | Asp | Phe |
| 110 | | | | | 115 | | | | | 120 | | | | | 125 |
| Leu | Leu | Asn | Tyr | Pro | Phe | Ser | Thr | Ser | Val | Lys | Leu | Ser | Thr | Gly | Cys |
| | | | | 130 | | | | | 135 | | | | | 140 | |
| Thr | Gly | Thr | Leu | Val | Ala | Glu | Lys | His | Val | Leu | Thr | Ala | Ala | His | Cys |
| | | | 145 | | | | | 150 | | | | | 155 | | |
| Ile | His | Asp | Gly | Lys | Thr | Tyr | Val | Lys | Gly | Thr | Gln | Lys | Leu | Arg | Val |
| | | 160 | | | | | 165 | | | | | 170 | | | |
| Gly | Phe | Leu | Lys | Pro | Lys | Phe | Lys | Asp | Gly | Gly | Arg | Gly | Ala | Asn | Asp |
| | 175 | | | | | 180 | | | | | 185 | | | | |
| Ser | Thr | Ser | Ala | Met | Pro | Glu | Gln | Met | Lys | Phe | Gln | Trp | Ile | Arg | Val |
| 190 | | | | | 195 | | | | | 200 | | | | | 205 |
| Lys | Arg | Thr | His | Val | Pro | Lys | Gly | Trp | Ile | Lys | Gly | Asn | Ala | Asn | Asp |
| | | | | 210 | | | | | 215 | | | | | 220 | |
| Ile | Gly | Met | Asp | Tyr | Asp | Tyr | Ala | Leu | Leu | Glu | Leu | Lys | Lys | Pro | His |
| | | | 225 | | | | 230 | | | | | | 235 | | |
| Lys | Arg | Lys | Phe | Met | Lys | Ile | Gly | Val | Ser | Pro | Pro | Ala | Lys | Gln | Leu |
| | | 240 | | | | | 245 | | | | | 250 | | | |
| Pro | Gly | Gly | Arg | Ile | His | Phe | Ser | Gly | Tyr | Asp | Asn | Asp | Arg | Pro | Gly |
| | 255 | | | | | 260 | | | | | 265 | | | | |
| Asn | Leu | Val | Tyr | Arg | Phe | Cys | Asp | Val | Lys | Asp | Glu | Thr | Tyr | Asp | Leu |
| 270 | | | | | 275 | | | | | 280 | | | | | 285 |
| Leu | Tyr | Gln | Gln | Cys | Asp | Ala | Gln | Pro | Gly | Ala | Ser | Gly | Ser | Gly | Val |
| | | | | 290 | | | | | 295 | | | | | 300 | |
| Tyr | Val | Arg | Met | Trp | Lys | Arg | Gln | Gln | Gln | Lys | Trp | Glu | Arg | Lys | Ile |
| | | | 305 | | | | | 310 | | | | | 315 | | |

Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro
320 325 330
Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln
335 340 345
Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly/Asp
350 355 360 365
Thr Val Phe Pro Pro Gly Ser Asn
370

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|------|
| ATGGCNGGNA | THCCNGGNYT | NYTNTTYT | YNTTYT | TNTGYC | NGTNGGNCAR | 60 |
| GTNWSNCCNT | AYWSNGCNCC | NTGGAARCCN | ACNTGGCCNG | CNTAYMGNYT | NCCNGTNGTN | 120 |
| YTNCNCARW | SNACNYTNAA | YYTNGCNAAR | CCNGAYTTYG | GNGCNGARGC | NAARYTNGAR | 180 |
| GTNWSNWSNW | SNTGYGGNCC | NCARTGYCAY | AARGGNACNC | CNYTNCCNAC | NTAYGARGAR | 240 |
| GCNAARCART | AYYTNWSNTA | YGARACNYTN | TAYGCNAAYG | GNWSNMGNAC | NGARACNCAR | 300 |
| GTNGGNATHT | AYATHYTNSW | NWSNWSNGGN | GAYGGNGCNC | ARCAYMGNGA | YWSNGGNWSN | 360 |
| WSNGGNAARW | SNMGNMGNAA | RMGNCARATH | TAYGGNTAYG | AYWSNMGNTT | YWSNATHTTY | 420 |
| GGNAARGAYT | TYYTNYTNAA | YTAYCCNTTY | WSNACNWSNG | TNAARYTNWS | NACNGGNTGY | 480 |
| ACNGGNACNY | TNGTNGCNGA | RAARCAYGTN | YTACNCGCNG | CNCAYTGYAT | HCAYGAYGGN | 540 |
| AARACNTAYG | TNAARGGNAC | NCARAARYTN | MGNGTNGGNT | TYYTNAARCC | NAARTTYAAR | 600 |
| GAYGGNGGNM | GNGGNGCNAA | YGAYWSNACN | WSNGCNATGC | CNGARCARAT | GAARTTYCAR | 660 |
| TGGATHMGNG | TNAARMGNAC | NCAYGTNCCN | AARGGNTGGA | THAARGGNAA | YGCNAAYGAY | 720 |
| ATHGGNATGG | AYTAYGAYTA | YGCNYTNYTN | GARYTNAAARA | ARCCNCAYAA | RMGNAARTTY | 780 |
| ATGAARATHG | GNGTNWSNCC | NCCNGCNAAR | CARYTNCCNG | GNGGNMGNAT | HCAYTTYWSN | 840 |
| GGNTAYGAYA | AYGAYMGNCC | NGGNAAYYT | GTNTAYMGNT | TYTGYGAYGT | NAARGAYGAR | 900 |
| ACNTAYGAYY | TNYTNTAYCA | RCARTGYGAY | GCNCARCCNG | GNGCNWSNGG | NWSNGGNGTN | 960 |
| TAYGTNMGNA | TGTGGAARMG | NCARCARCAR | AARTGGGARM | GNAARATHAT | HGGNATHTTY | 1020 |
| WSNGGNCAYC | ARTGGGTNGA | YATGAAYGGN | WSNCCNCARG | AYTTYAAYGT | NGCNGTNMGN | 1080 |
| ATHACNCCNY | TNAARTAYGC | NCARATHTG | TAYTGGATHA | ARGGNAAYTA | YYTNGAYTGY | 1140 |
| MGNGARGGNG | AYACNGTNTT | YCCNCCNGGN | WSNAAY | | | 1176 |